

RE-RUN



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,054A

DATE: 08/10/2004

TIME: 15:07:55

Input Set : A:\TPP31440.txt

Output Set: N:\CRF4\08102004\J088054A.raw

3 <110> APPLICANT: Deleersnijder, Willy
 4 Nys, Guy
 5 D'Heuvaert, Nicole
 6 van Tetering, Angelique
 7 Sloothaak, Jan Bart
 8 Frankena, Jurjen
 9 Venema, Jakob
 11 <120> TITLE OF INVENTION: Novel Human G-Protein coupled Receptor
 13 <130> FILE REFERENCE: TPP 31440
 15 <140> CURRENT APPLICATION NUMBER: US 10/088,054A
 16 <141> CURRENT FILING DATE: 2002-03-14
 18 <160> NUMBER OF SEQ ID NOS: 9
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1176
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (149)..(1138)
 31 <400> SEQUENCE: 1
 32 ttaatctctt caagcctctg atttctcttc ctgtaaaaca ggggcggtaa ttaccacata 60
 34 acaggctggt catgaaaatc agtgaacatg cagcaggtgc tcaagtcttg tttttgttc 120
 36 caggggcacc agtggaggtt ttctgagc atg gat cca acc acc ccg gcc tgg 172
 37 Met Asp Pro Thr Thr Pro Ala Trp
 38
 40 gga aca gaA agt aca aca gtg aat gga aat gac caa gcc ctt ctt ctg 220
 41 Gly Thr Glu Ser Thr Thr Val Asn Gly Asn Asp Gln Ala Leu Leu Leu
 42 10 15 20
 44 ctt tgt ggc aag gag acc ctg atc ccg gtc ttc ctg atc ctt ttc att 268
 45 Leu Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile
 46 25 30 35 40
 48 gcc ctg gtc ggg ctg gta gga aac ggg ttt gtg ctc tgg ctc ctg ggc 316
 49 Ala Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly
 50 45 50 55
 52 ttc cgc atg cgc agg aac gcc ttc tct gtc tac gtc ctc agc ctg gcc 364
 53 Phe Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala
 54 60 65 70
 56 ggg gcc gac ttc ctc ttc ctc tgc ttc cag att ata aat tgc ctg gtg 412
 57 Gly Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val
 58 75 80 85
 60 tac ctc agt aac ttc ttc tgt tcc atc tcc atc aat ttc cct agc ttc 460
 61 Tyr Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe

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62      90      95      100
64 ttc acc act gtg atg acc tgt gcc tac ctt gca ggc ctg agc atg ctg 508
65 Phe Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu
66 105      110      115      120
68 agc acc gtc agc acc gag cgc tgc ctg tcc gtc ctg tgg ccc atc tgg 556
69 Ser Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp
70      125      130      135
72 tat cgc tgc cgc cgc ccc aga cac ctg tca gcg gtc gtg tgt gtc ctg 604
73 Tyr Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu
74      140      145      150
76 ctc tgg gcc ctg tcc cta ctg ctg agc atc ttg gaa ggg aag ttc tgt 652
77 Leu Trp Ala Leu Ser Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys
78      155      160      165
80 ggc ttc tta ttt agt gat ggt gac tct ggt tgg tgt cag aca ttt gat 700
81 Gly Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp
82      170      175      180
84 ttc atc act gca gcg tgg ctg att ttt tta ttc atg gtt ctc tgt ggg 748
85 Phe Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly
86 185      190      195      200
88 tcc agt ctg gcc ctg ctg gtc agg atc ctc tgt ggc tcc agg ggt ctg 796
89 Ser Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu
90      205      210      215
92 cca ctg acc agg ctg tac ctg acc atc ctg ctc aca gtg ctg gtg ttc 844
93 Pro Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Phe
94      220      225      230
96 ctc ctc tgc ggc ctg ccc ttt ggc att cag tgg ttc cta ata tta tgg 892
97 Leu Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp
98      235      240      245
100 atc tgg aag gat tct gat gtc tta ttt tgt cat att cat cca gtt tca 940
101 Ile Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser
102      250      255      260
104 gtt gtc ctg tca tct ctt aac agc agt gcc aac ccc atc att tac ttc 988
105 Val Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe
106 265      270      275      280
108 ttc gtg ggc tct ttt agg aag cag tgg cgg ctg cag cag ccg atc ctc 1036
109 Phe Val Gly Ser Phe Arg Lys Gln Trp Arg Leu Gln Gln Pro Ile Leu
110      285      290      295
112 aag ctg gct ctc cag agg gct ctg cag gac att gct gag gtg gat cac 1084
113 Lys Leu Ala Leu Gln Arg Ala Leu Gln Asp Ile Ala Glu Val Asp His
114      300      305      310
116 agt gaa gga tgc ttc cgt cag ggc acc ccg gag atg tcg aga agc agt 1132
117 Ser Glu Gly Cys Phe Arg Gln Gly Thr Pro Glu Met Ser Arg Ser Ser
118      315      320      325
120 ctg gtg tagagatgga cagcctctac ttccatcaga tatatgtg 1176
121 Leu Val
122      330
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 330
127 <212> TYPE: PRT

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128 <213> ORGANISM: Homo sapiens
130 <400> SEQUENCE: 2
131 Met Asp Pro Thr Thr Pro Ala Trp Gly Thr Glu Ser Thr Thr Val Asn
132 1 5 10 15
134 Gly Asn Asp Gln Ala Leu Leu Leu Leu Cys Gly Lys Glu Thr Leu Ile
135 20 25 30
137 Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val Gly Asn
138 35 40 45
140 Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe
141 50 55 60
143 Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys
144 65 70 75 80
146 Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser
147 85 90 95
149 Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala
150 100 105 110
152 Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys
153 115 120 125
155 Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg Pro Arg His
156 130 135 140
158 Leu Ser Ala Val Val Cys Val Leu Leu Trp Ala Leu Ser Leu Leu Leu
159 145 150 155 160
161 Ser Ile Leu Glu Gly Lys Phe Cys Gly Phe Leu Phe Ser Asp Gly Asp
162 165 170 175
164 Ser Gly Trp Cys Gln Thr Phe Asp Phe Ile Thr Ala Ala Trp Leu Ile
165 180 185 190
167 Phe Leu Phe Met Val Leu Cys Gly Ser Ser Leu Ala Leu Leu Val Arg
168 195 200 205
170 Ile Leu Cys Gly Ser Arg Gly Leu Pro Leu Thr Arg Leu Tyr Leu Thr
171 210 215 220
173 Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly
174 225 230 235 240
176 Ile Gln Trp Phe Leu Ile Leu Trp Ile Trp Lys Asp Ser Asp Val Leu
177 245 250 255
179 Phe Cys His Ile His Pro Val Ser Val Val Leu Ser Ser Leu Asn Ser
180 260 265 270
182 Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg Lys Gln
183 275 280 285
185 Trp Arg Leu Gln Gln Pro Ile Leu Lys Leu Ala Leu Gln Arg Ala Leu
186 290 295 300
188 Gln Asp Ile Ala Glu Val Asp His Ser Glu Gly Cys Phe Arg Gln Gly
189 305 310 315 320
191 Thr Pro Glu Met Ser Arg Ser Ser Leu Val
192 325 330
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 26
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:

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202 <223> OTHER INFORMATION: Description of Artificial Sequence: Degenerated
203 primers
205 <220> FEATURE:
206 <221> NAME/KEY: variation
207 <222> LOCATION: (21)
208 <223> OTHER INFORMATION: A,C,G or T
210 <220> FEATURE:
211 <221> NAME/KEY: variation
212 <222> LOCATION: (24)
213 <223> OTHER INFORMATION: A,C,G or T
215 <400> SEQUENCE: 3
W--> 216 ctgcactacc acgtgetcws nytngc 26
219 <210> SEQ ID NO: 4
220 <211> LENGTH: 28
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Artificial Sequence: Degenerated
226 primers
228 <220> FEATURE:
229 <221> NAME/KEY: variation
230 <222> LOCATION: (21)
231 <223> OTHER INFORMATION: A,C,G or T
233 <220> FEATURE:
234 <221> NAME/KEY: variation
235 <222> LOCATION: (27)
236 <223> OTHER INFORMATION: C or Inosine
238 <400> SEQUENCE: 4
W--> 239 ggggtggcaga tggccarrya nckytcnb 28
242 <210> SEQ ID NO: 5
243 <211> LENGTH: 31
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Degenerated
249 primers
251 <220> FEATURE:
252 <221> NAME/KEY: variation
253 <222> LOCATION: (25)
254 <223> OTHER INFORMATION: A,C,G or T
256 <400> SEQUENCE: 5
W--> 257 gtggcagatg gccaggcagc grtcnrcrct d 31
260 <210> SEQ ID NO: 6
261 <211> LENGTH: 28
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
268 <400> SEQUENCE: 6

RAW SEQUENCE LISTING

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Input Set : A:\TPP31440.txt

Output Set: N:\CRF4\08102004\J088054A.raw

269 ggggccgact tcctcttcct ctgcttcc 28
272 <210> SEQ ID NO: 7
273 <211> LENGTH: 28
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
280 <400> SEQUENCE: 7
281 gcaaggtagg cacaggtcat cacagtgg 28
284 <210> SEQ ID NO: 8
285 <211> LENGTH: 31
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
292 <400> SEQUENCE: 8
293 ataagcttct ccctggccct taataaatga c 31
296 <210> SEQ ID NO: 9
297 <211> LENGTH: 29
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
304 <400> SEQUENCE: 9
305 aggaattcag acagacaggg gcaaagttg 29

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/088,054A

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TIME: 15:07:57

Input Set : A:\TPP31440.txt
Output Set: N:\CRF4\08102004\J088054A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 21,24

Seq#:4; N Pos. 21,27

Seq#:5; N Pos. 25

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,054A

DATE: 08/10/2004

TIME: 15:07:57

Input Set : A:\TPP31440.txt

Output Set: N:\CRF4\08102004\J088054A.raw

L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0